



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 184136

**TO: Patrick S Riggins
Location: REM-2D60&2C70
Art Unit: 1633
Monday, April 10, 2006
Case Serial Number: 10/500173**

**From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523
toby.port@uspto.gov**

Search Notes

Examiner Riggins,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

**Toby Port
X22523**

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:10:27 ; Search time 344.814 Seconds
(without alignments)
6758.955 Million cell updates/sec

Title: US-10-500-173-1
Perfect score: 41
Sequence: 1 gaacaatgacacatcgc.....cccaatacaggcctgac 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	41	6	BD181246 Cell spec
2	41	100.0	41	6	BD182147 Cell spec
3	41	100.0	260	6	BD182147 Cell spec
4	41	100.0	260	6	BD182148 Cell spec
5	41	100.0	314	8	BD182148 Cell spec
6	41	100.0	333	6	BD181248 Cell spec
7	41	100.0	333	6	BD182149 Cell spec
8	41	100.0	1221	8	BD5611 Human smoot
9	41	100.0	142645	8	AC008481 Homo sapi
10	41	100.0	178488	14	AC151856
11	41	100.0	224294	14	AC151861
12	39.4	96.1	163264	14	AC151891
13	39.4	96.1	181714	14	AC151893
14	39.4	96.1	186803	14	AC151868
15	39.4	96.1	195562	14	AC163457
16	39.4	96.1	250810	14	AC151886
17	37.8	92.2	236017	14	AC150437
18	36.2	88.3	485	9	AF123268

19	36.2	88.3	1216	9	MMCALP01	CR628386	Mus musculus
20	36.2	88.3	3001	9	MMU37071	AC098590	Mus musculus
21	36.2	88.3	10373	9	MUSHLCA	AC027417	Mus musculus
22	36.2	88.3	174533	14	AC073718	AC048384	Mus musculus
23	36.2	88.3	178594	14	AC144892	AC148218	Mus musculus
24	36.2	88.3	194267	14	AC163623	AC114696	Mus musculus
25	36.2	88.3	195294	14	AC051623	AC125214	Mus musculus
26	36.2	88.3	201371	14	AC073786	AC18766	Mus musculus
27	36.2	88.3	235685	14	AC084744	AC118766	Mus musculus
28	36.2	88.3	245942	14	AC132792	AC111714	Mus musculus
29	34.6	84.4	207823	14	AC145542	AC002243	Mus musculus
30	25.6	62.4	230705	14	AC130996	Chlamydom	
31	24.2	59.0	171632	8	AC110760		
32	24.2	59.0	220801	9	AC124604		
33	24	58.5	263827	14	AC095809		
34	23.6	57.6	110000	1	BA000031_19		
35	23.6	57.6	133128	5	BX276083		
36	23.6	57.6	149630	14	CR628386		
37	23.6	57.6	153943	14	AC027417		
38	23.6	57.6	157544	8	AC098590		
39	23.6	57.6	170143	14	AC048384		
40	23.2	56.6	58259	14	AC148218		
41	23.2	56.6	209156	14	AC114696		
42	23.2	56.6	214942	9	AC125214		
43	23.2	56.6	227767	14	AC118766		
44	23.2	56.6	228506	14	AC111714		
45	23	56.1	9990	1	AE002243		

ALIGNMENTS

RESULT 1
BD181246
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 41)
Takahashi, K., Yamamura, H. and Miyatake, S.
Cell specific express replication vector
Patent: JP 2002335965-A 1 26-NOV-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002335965-A/1
PD 26-NOV-2002
PF 14-MAY-2001 JP 2001143999
PI KATSUHIRO TAKAHASHI, HISAKO YAMAMURA, SHINICHI MIYATAKE PC
C12N15/09, A61K35/76, A61K48/00, A61P35/00, C12N5/10, C12N15/00, PC
C12N5/00
CC Cell specific express replication vector
FH Key
FT source
FT Location/Qualifiers
1. .41
/organism="Homo sapiens (human)"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Score 41; DB 6; Length 41;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAATGACACATCAGCTCCCAATACCAAGGCGCTGAC 41

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:04:37 ; Search time 59.4306 Seconds
(without alignment)
4597.840 Million cell updates/sec

Title: US-10-500-173-1
Perfect score: 41
Sequence: 1 gaaacaatgacacatcagc.....cccaatacaggccctgac 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001as.*

5: Geneseq2001bs.*

6: Geneseq2002as.*

7: Geneseq2002bs.*

8: Geneseq2003as.*

9: Geneseq2003bs.*

10: Geneseq2003cs.*

11: Geneseq2003ds.*

12: Geneseq2004as.*

13: Geneseq2004bs.*

14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	41	100.0	41	10	ADC21270	Adc21270 Human ang
2	41	100.0	41	10	ADD68309	Add68309 Human ang
3	41	100.0	41	10	ADD29393	Add29393 Antiarter
4	41	100.0	41	10	ABZ70044	Abz70044 Oligonuc1
5	41	100.0	260	10	ADC21271	Adc21271 Human cel
6	41	100.0	260	10	ADD68310	Add68310 Human ang
7	41	100.0	260	10	ADD29394	Add29394 Antiarter
8	41	100.0	260	10	ABZ70045	Abz70045 Oligonuc1
9	41	100.0	333	10	ADC21272	Adc21272 Human cel
10	41	100.0	333	10	ADD68311	Add68311 DNA compr
11	41	100.0	333	10	ADD29395	Add29395 Human cel
12	41	100.0	333	10	ABZ70046	Abz70046 Human cel
C 13	23	56.1	110000	2	AAK91990_11	Continuation (12 o
C 14	22.2	54.1	780	8	ACA40205	Aca40205 Prokaryot
15	22	53.7	652	2	AAK19896	Aax19896 Mouse pro
16	22	53.7	2293	2	AAK19900	Aax19900 Plasmid p
C 17	21.8	53.2	168276	11	ACN43942	Acn43942 Human gen
18	21.6	52.7	86131	10	ADF77178	Adf77178 KALPA gen
19	21.4	52.2	1209	9	ADB85463	Adb85463 Streptoco

20	21.4	52.2	1212	9	ADB85471	Adb85471 Streptoco
21	21.4	52.2	4226	4	ABL08190	Abi08190 Drosophil
C 22	21.4	52.2	110000	14	AEA61163_2	Continuation (3 of
23	21.2	51.7	957	8	ABX92193	Abx92193 Human ova
24	21.2	51.7	1460	8	ABX92194	Abx92194 Human ova
25	21.2	51.7	64125	13	ABD33295	Abd33295 Human can
26	21	51.2	396	8	ABX47703	Abx47703 Bovine ES
27	21	51.2	403	8	ABX40611	Abx40611 Bovine ES
C 28	21	51.2	417	3	AAC41719	Aac41719 Arabidops
C 29	21	51.2	616	3	AAC44877	Aac44877 Arabidops
30	21	51.2	753	8	ABX05433	Abx05433 Human nov
31	21	51.2	803	6	ABQ26745	Abq26745 Oligonuc1
C 32	21	51.2	803	6	ABQ26744	Abq26744 Oligonuc1
C 33	21	51.2	972	5	AAS66748	Aas66748 DNA encod
34	21	51.2	973	6	ABN74450	Abn74450 Bovine em
35	21	51.2	974	6	ABN74449	Abn74449 Bovine em
36	21	51.2	1270	2	AAZ24855	Aaz24855 Human sec
37	21	51.2	11445	4	AAK70537	Aak70537 Human imm
C 38	21	51.2	46830	14	ADZ12773	Adz12773 Human can
C 39	21	51.2	55235	4	AAK67426	Aak67426 Human imm
C 40	21	51.2	73930	12	ADQ97577	Adq97577 Human can
C 41	21	51.2	86574	6	ABK83560	Abk83560 Human CDN
C 42	21	51.2	86574	13	ADZ52822	Adz52822 Drug ther
C 43	20.8	50.7	180	6	ABQ95988	Abq95988 Tumour su
C 44	20.8	50.7	199	6	ABQ95990	Abq95990 Tumour su
C 45	20.8	50.7	199	6	ABQ95984	Abq95984 Tumour su

ALIGNMENTS

RESULT 1
ADC21270

ID ADC21270 standard; DNA; 41 BP.

XX
AC ADC21270;

DT 18-DEC-2003 (first entry)

XX
DE Human cell-specific expression vector-related DNA sequence #1.

XX
KW human; cell-specific expression vector; cell-specific replication vector;
KW gene therapy; malignant tumour; liver fibrosis; postoperative stenosis;
KW organ transplantation; arteriosclerosis; diabetic omentopathy; ds.

XX
OS Homo sapiens.

XX
PN WO2003057888-A1.

XX
PD 17-JUL-2003.

XX
PF 26-DEC-2002; 2002WO-JP013683.

XX
PR 28-DEC-2001; 2001JP-00402102.

XX
PR 30-AUG-2002; 2002JP-00255395.

XX
(NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX
Takahashi K, Yamamura H;

XX
WPI; 2003-577527/54.

XX
Cell-specific expression/replication vector containing transcription
PT initiation regulating domain of human calponin gene, applicable in gene
PT therapy of malignant tumor lung and liver fibrosis or diabetic
PT omentopathy.

XX
Claim 2; SEQ ID NO 1; 66pp; Japanese.

XX
The invention comprises a cell-specific expression/replication vector
CC which does not act on normal cells. The vector of the invention is useful
CC in gene therapy for the treatment of: malignant tumour, liver fibrosis,
CC postoperative stenosis (e.g. stenosis after organ transplantation),

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:12:09 ; Search time 421.382 Seconds
 (without alignments)
 4552.334 Million cell updates/sec

Title: US-10-500-173-1

Perfect score: 41

Sequence: 1 gaacaatgacacaatcagc.....cccaataccaggcctgac 41

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est2:*
 3: gb_est3:*
 4: gb_hic:*
 5: gb_est4:*
 6: gb_est5:*
 7: gb_est6:*
 8: gb_est7:*
 9: gb_ges1:*
 10: gb_ges2:*
 11: gb_ges3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24.2	59.0	578	9	AZ954724 2M0220101
C 2	24.2	59.0	687	2	BB636361
C 3	24.2	59.0	817	8	CX705842 gmtcdxns0
C 4	24.2	58.5	578	2	BG887927 EST513778
C 5	23.2	56.6	455	8	W81232 zds507.e1
C 6	23.2	56.6	457	8	DN589073 49998.1 L
C 7	23.2	56.6	457	8	DR037737 49998.2 L
C 8	23.2	56.6	457	8	DR037738 49998.3 L
C 9	23.2	56.6	465	1	A1773494 EST254594
C 10	23.2	56.6	580	1	A1170292 EST216218
C 11	23.2	56.6	624	2	BQ046841 EST503788
C 12	23.2	56.6	736	3	BQ046841 EST503788
C 13	23.2	56.1	403	6	CD002122 EST0119 N
C 14	23.2	56.1	429	6	CD603495 Z148A3B0
C 15	23.2	56.1	444	3	BM403754 zam6160 Z
C 16	23.2	56.1	486	5	BW881674 BW881674
C 17	23.2	56.1	489	2	BG799583 f08h03.Y
C 18	23.2	56.1	571	9	AQ891537 HS 3063 A
C 19	23.2	56.1	644	6	CB343759 CA32EN00
C 20	23.2	56.1	732	6	CF232494 PtaXO001
C 21	23.2	56.1	760	9	BZ773739 mcv78b08.
C 22	23.2	56.1	1246	10	AG341458 Mus muscu

CB577767 AMGNNUC.U
 CW332222 104 829 1
 CW332223 104 829 1
 DR917045 EST110858
 BZ988727 PUGHP347B
 CC350006 OGIA911TH
 CG106814 PUFVE867B
 CU292836 ZMMBBB064
 CC364981 PUEEC65TD
 BU035599 QHJ7H13.Y
 BG591195 EST499037
 DN842758 KECB32-27
 CO908605 BU02033B1
 AQ061197 CIT-HSP-2
 CR490303 mth2-1610
 CR038246 Forward 8
 CR259602 Forward 8
 BE343332 EST408481
 BE344046 EST409208
 CA947544 EST0452 C
 BU021048 QHE29C11.
 CO911511 BJ0302081
 BE920230 EST423959

22.8 55.6 628 6 CB577767
 22.8 55.6 697 10 CW332222
 22.8 55.6 750 10 CW332223
 22.6 55.1 420 8 DR917045
 22.6 55.1 822 9 BZ988727
 22.6 55.1 861 9 CC350006
 22.6 55.1 869 10 CG106814
 22.6 55.1 883 10 CU292836
 22.6 55.1 908 9 CC364981
 22.4 54.6 137 5 BU035599
 22.4 54.6 233 2 BG591195
 22.4 54.6 323 8 DN842758
 22.4 54.6 358 7 CO908605
 22.4 54.6 386 9 AQ061197
 22.4 54.6 402 11 CR490303
 22.4 54.6 424 11 CR038246
 22.4 54.6 425 11 CR259602
 22.4 54.6 438 2 BE343332
 22.4 54.6 453 2 BE344046
 22.4 54.6 474 6 CA947544
 22.4 54.6 478 5 BU021048
 22.4 54.6 487 7 CO911511
 22.4 54.6 490 2 BE920230

RESULT 1
 AZ954724/c
 LOCUS
 DEFINITION 2M0220101R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0220101 R, genomic survey sequence.
 ACCESSION AZ954724
 VERSION AZ954724.1 GI:13825951
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
 1 (bases 1 to 578)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0220 row: I column: 01
 Seq primer: CACACGAGAACCTATGACC
 Class: plasmid ends
 High quality sequence stop: 578.
 Location/Qualifiers
 1..578
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0220101"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="vector: PWD42nv; Purified genomic DNA from M.

ALIGNMENTS

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 13:46:44 ; Search time 20.1767 Seconds
(without alignments)
3612.096 Million cell updates/sec

Title: US-10-500-173-1

Perfect score: 41

Sequence: 1 gaacaatgacacaaatcagc.....cccaataccaggccctgac 41

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	15585	3	US-09-949-016-11927, A
2	41	100.0	15585	3	US-09-949-016-15627, A
3	23	56.1	1230025	3	US-09-198-452A-1
4	23	56.1	1230230	3	US-09-438-185A-1
5	21.8	53.2	601	3	US-09-949-016-130708
6	21.8	53.2	42250	3	US-09-949-016-15426
7	21.6	52.7	601	3	US-09-949-016-196661
8	21.6	52.7	28585	3	US-09-949-016-17311
9	21	51.2	209210	3	US-09-949-016-15094
10	20.8	50.7	456	3	US-09-328-352-82
11	20.8	50.7	601	3	US-09-949-016-103354
12	20.8	50.7	601	3	US-09-949-016-103355
13	20.8	50.7	601	3	US-09-949-016-127545
14	20.8	50.7	723	3	US-09-328-352-298
15	20.8	50.7	2904	3	US-09-054-272-29
16	20.8	50.7	4450	3	US-09-949-016-2850
17	20.8	50.7	4510	3	US-09-919-039-16
18	20.8	50.7	34531	3	US-09-949-016-14604
19	20.8	50.7	36223	3	US-09-949-016-14417
20	20.8	50.7	73757	3	US-09-949-016-15369
21	20.6	50.2	50109	3	US-09-949-016-14112
22	20.6	50.2	98708	3	US-09-949-016-16392
23	20.4	49.8	601	3	US-09-949-016-64221
24	20.4	49.8	981	3	US-09-270-767-956

c	25	20.4	49.8	981	3	US-09-270-767-16238	Sequence 16238, A
	26	20.4	49.8	88906	3	US-09-949-016-17468	Sequence 17468, A
	27	20.4	49.8	106746	3	US-09-326-402C-1	Sequence 1, Appli
	28	20.4	49.8	106746	3	US-09-326-402C-12	Sequence 12, Appli
c	29	20.4	49.8	183202	3	US-09-949-016-13614	Sequence 13614, A
	30	20.4	49.8	818128	3	US-09-949-016-14546	Sequence 14546, A
	31	20.4	49.8	818128	3	US-09-949-016-14547	Sequence 14547, A
	32	20.4	49.8	818128	3	US-09-949-016-14548	Sequence 14548, A
	33	20.4	49.8	818128	3	US-09-949-016-14549	Sequence 14549, A
	34	20.4	49.8	818128	3	US-09-949-016-14550	Sequence 14550, A
	35	20.4	49.8	818128	3	US-09-949-016-14551	Sequence 14551, A
	36	20.4	49.8	818128	3	US-09-949-016-14552	Sequence 14552, A
	37	20.4	49.8	818128	3	US-09-949-016-14553	Sequence 14553, A
	38	20.4	49.8	818128	3	US-09-949-016-14554	Sequence 14554, A
	39	20.4	49.8	818128	3	US-09-949-016-14555	Sequence 14555, A
	40	20.4	49.8	818128	3	US-09-949-016-14556	Sequence 14556, A
	41	20.4	49.8	818128	3	US-09-949-016-14557	Sequence 14557, A
	42	20.4	49.8	818128	3	US-09-949-016-14558	Sequence 14558, A
	43	20.4	49.8	818128	3	US-09-949-016-14559	Sequence 14559, A
	44	20.4	49.8	818128	3	US-09-949-016-14560	Sequence 14560, A
	45	20.4	49.8	818128	3	US-09-949-016-14561	Sequence 14561, A

ALIGNMENTS

RESULT 1

US-09-949-016-11927
; Sequence 11927, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11927
; LENGTH: 15585
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(15585)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11927

Query Match 100.0%; Score 41; DB 3; Length 15585;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAATGACACAAATCAGCTCCCAATACCAAGGCGCTGAC 41
|||||
DB 1819 GAACAATGACACAAATCAGCTCCCAATACCAAGGCGCTGAC 1859

RESULT 2

US-09-949-016-15627
; Sequence 15627, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:22:52 ; Search time 96.2918 Seconds
(without alignments)
3521.011 Million cell updates/sec

Title: US-10-500-173-1
Perfect score: 41
Sequence: 1 gaacaatgacacatcagc.....cccaatacgaaggcctgac 41

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq.*
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7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq.*
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9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	41	100.0	41	8	US-10-500-173-1	8	Sequence 1, Appli
2	41	100.0	41	8	US-10-500-173-1	8	Sequence 1, Appli
3	41	100.0	260	8	US-10-477-797-2	2	Sequence 1, Appli
4	41	100.0	260	8	US-10-500-173-2	2	Sequence 1, Appli
5	41	100.0	333	8	US-10-477-797-3	3	Sequence 1, Appli
6	41	100.0	333	8	US-10-500-173-3	3	Sequence 1, Appli
C 7	24.2	59.0	297	7	US-10-424-599-2981	7	Sequence 2981, Ap
C 8	23.6	57.6	616	4	US-09-925-065A-836727	4	Sequence 836727, Ap
C 9	23	56.1	1230025	6	US-10-289-762-1	1	Sequence 1, Appli
10	22.6	55.1	554	5	US-10-027-632-265758	5	Sequence 265758, Ap
11	22.6	55.1	554	5	US-10-027-632-265759	5	Sequence 265759, Ap
12	22.6	55.1	554	5	US-10-027-632-265758	5	Sequence 265758, Ap
13	22.6	55.1	554	5	US-10-027-632-265758	5	Sequence 265758, Ap
14	22.6	55.1	554	5	US-10-027-632-265759	5	Sequence 265759, Ap
15	22.6	55.1	554	5	US-10-027-632-265760	5	Sequence 265760, Ap
C 16	22.4	54.6	472	4	US-09-925-065A-591662	4	Sequence 591662, Ap
C 17	22.4	54.6	472	4	US-09-925-065A-591663	4	Sequence 591663, Ap
18	22.4	54.6	526	5	US-10-027-632-273806	5	Sequence 273806, Ap
19	22.4	54.6	526	5	US-10-027-632-273806	5	Sequence 273806, Ap
20	22.4	54.6	530	4	US-09-925-065A-592112	4	Sequence 592112, Ap
21	22.4	54.6	530	4	US-09-925-065A-592113	4	Sequence 592113, Ap
22	22.4	54.6	530	4	US-09-925-065A-592114	4	Sequence 592114, Ap
C 23	22.4	54.6	574	4	US-09-925-065A-411954	4	Sequence 411954, Ap

Sequence 16888, A
Sequence 28075, A
Sequence 113737, A
Sequence 592115, A
Sequence 148088, A
Sequence 135928, A
Sequence 142, App
Sequence 90554, A
Sequence 652206, A
Sequence 88682, A
Sequence 90555, A
Sequence 802711, A
Sequence 856292, A
Sequence 856293, A
Sequence 856294, A
Sequence 892774, A
Sequence 870115, A
Sequence 5, Appli
Sequence 13, Appli
Sequence 97711, A
Sequence 97711, A
Sequence 9526, Ap

24 22.2 54.1 333 8 US-10-425-115-16888
25 22.2 54.1 780 7 US-10-282-122A-28075
26 22.2 54.1 1075 8 US-10-425-115-113737
27 22 53.7 530 4 US-09-925-065A-592115
28 21.8 53.2 2539 8 US-10-425-115-148088
29 21.8 53.2 2546 7 US-10-424-599-135928
30 21.6 53.2 168276 5 US-10-087-192-142
31 21.6 52.7 518 7 US-10-424-599-90554
32 21.6 52.7 603 4 US-09-925-065A-652206
33 21.6 52.7 1331 4 US-09-925-065A-88682
34 21.6 52.7 1852 7 US-10-424-599-90555
35 21.4 52.2 507 4 US-09-925-065A-802711
36 21.4 52.2 507 4 US-09-925-065A-856292
37 21.4 52.2 507 4 US-09-925-065A-856293
38 21.4 52.2 507 4 US-09-925-065A-856294
39 21.4 52.2 577 4 US-09-925-065A-892774
40 21.4 52.2 595 4 US-09-925-065A-870115
41 21.4 52.2 1209 6 US-10-284-400-5
42 21.4 52.2 1212 6 US-10-284-400-13
43 21.4 52.2 1839 5 US-10-027-632-97711
44 21.4 52.2 1839 6 US-10-027-632-97711
45 21.4 52.2 4226 10 US-11-097-143-9526

ALIGNMENTS

RESULT 1

US-10-477-797-1

Sequence 1, Application US/10477797

Publication No. US20040197308A1

GENERAL INFORMATION:

APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION

TITLE OF INVENTION: Replication Vector Showing Cell-Specific Expression

FILE REFERENCE: K01002PCT

CURRENT APPLICATION NUMBER: US/10/477,797

CURRENT FILING DATE: 2003-11-13

PRIOR APPLICATION NUMBER: JP P2001-143999

PRIOR FILING DATE: 2001-05-14

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 41

TYPE: DNA

ORGANISM: Homo sapiens

US-10-477-797-1

Query Match 100.0%; Score 41; DB 8; Length 41;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAATGACACATCAGCTCCCAATACCAAGGCCTGAC 41
Db 1 GAACAATGACACATCAGCTCCCAATACCAAGGCCTGAC 41

RESULT 2

US-10-500-173-1

Sequence 1, Application US/10500173

Publication No. US20050032214A1

GENERAL INFORMATION:

APPLICANT: Katsuhito TAKAHASHI

APPLICANT: Hisako YAMAMURA

TITLE OF INVENTION: Cell specific expression/replication vector

FILE REFERENCE: 4439-4022

CURRENT APPLICATION NUMBER: US/10/500,173

CURRENT FILING DATE: 2004-06-24

PRIOR APPLICATION NUMBER: JP P2001-402102

PRIOR FILING DATE: 2001-12-28

PRIOR APPLICATION NUMBER: JP P2002-255395

PRIOR FILING DATE: 2002-08-30

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Ver. 2.1

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:36:12 ; Search time 75.6625 Seconds
(without alignments)
2167.823 Million cell updates/sec

Title: US-10-500-173-1
Perfect score: 41
Sequence: 1 gaacaatgacacacacgc.....cccaatacaggcctgac 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Number of hits satisfying chosen parameters: 18535810

num DB seq length: 0

num DB seq length: 200000000

processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDSS/ptodata/1/pubpna/US06_NEW_PUB.seq:
3: /SIDSS/ptodata/1/pubpna/US07_NEW_PUB.seq:
4: /SIDSS/ptodata/1/pubpna/US09_NEW_PUB.seq:
5: /SIDSS/ptodata/1/pubpna/US09_NEW_PUB.seq:
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7: /SIDSS/ptodata/1/pubpna/US10_NEW_PUB.seq:
8: /SIDSS/ptodata/1/pubpna/US10_NEW_PUB.seq:
9: /SIDSS/ptodata/1/pubpna/US10_NEW_PUB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	23	56.1	13187	US-11-136-527-4095	Sequence 4095, Ap
C 3	22.6	55.1	554	US-10-301-480-100586	Sequence 100586
C 4	22.6	55.1	554	US-10-301-480-100587	Sequence 100587
C 5	22.6	55.1	554	US-10-301-480-100588	Sequence 100588
C 6	22.6	55.1	554	US-10-301-480-100589	Sequence 100589
C 7	22.6	55.1	554	US-10-301-480-100590	Sequence 100590
C 8	22.6	55.1	554	US-10-301-480-100591	Sequence 100591
C 9	22.6	55.1	554	US-10-301-480-100592	Sequence 100592
C 10	22.4	54.6	472	US-09-925-065A-591662	Sequence 591662
C 11	22.4	54.6	530	US-09-925-065A-591663	Sequence 591663
C 12	22.4	54.6	530	US-09-925-065A-592112	Sequence 592112
C 13	22.4	54.6	530	US-09-925-065A-592113	Sequence 592113
C 14	22.4	54.6	558	US-10-301-480-509257	Sequence 509257
C 15	22.4	54.6	558	US-10-301-480-509258	Sequence 509258
C 16	22.4	54.6	558	US-10-301-480-509259	Sequence 509259
C 17	22.4	54.6	558	US-10-301-480-1122666	Sequence 1122666
C 18	22.4	54.6	558	US-10-301-480-1122667	Sequence 1122667

C 19	22.4	54.6	558	10	US-10-301-480-1122668	Sequence 1122668
C 20	22.4	54.6	574	6	US-09-925-065A-411954	Sequence 411954
C 21	22.4	54.6	575	10	US-10-301-480-478094	Sequence 478094
C 22	22.4	54.6	578	10	US-10-301-480-1091503	Sequence 1091503
C 23	22	53.7	530	6	US-09-925-065A-592115	Sequence 592115
C 24	21.6	52.7	603	6	US-09-925-065A-592115	Sequence 592115
C 25	21.6	52.7	1331	6	US-09-925-065A-592115	Sequence 592115
C 26	21.6	52.7	1331	9	US-10-301-480-189923	Sequence 189923
C 27	21.6	52.7	1331	10	US-10-301-480-189923	Sequence 189923
C 28	21.6	52.7	1435	8	US-10-301-480-803332	Sequence 803332
C 29	21.6	52.7	1435	8	US-10-750-185-52319	Sequence 52319, A
C 30	21.4	52.2	507	6	US-09-925-065A-802711	Sequence 802711, A
C 31	21.4	52.2	507	6	US-09-925-065A-856292	Sequence 856292
C 32	21.4	52.2	507	6	US-09-925-065A-856293	Sequence 856293
C 33	21.4	52.2	507	6	US-09-925-065A-856294	Sequence 856294
C 34	21.4	52.2	577	6	US-09-925-065A-892774	Sequence 892774
C 35	21.4	52.2	595	6	US-09-925-065A-870115	Sequence 870115
C 36	21.4	52.2	856	10	US-10-301-480-545231	Sequence 545231
C 37	21.4	52.2	856	10	US-10-301-480-545232	Sequence 545232
C 38	21.4	52.2	856	10	US-10-301-480-1158640	Sequence 1158640
C 39	21.4	52.2	856	10	US-10-301-480-1158641	Sequence 1158641
C 40	21.4	52.2	864	10	US-10-301-480-545605	Sequence 545605
C 41	21.4	52.2	864	10	US-10-301-480-1159014	Sequence 1159014
C 42	21.2	51.7	1015	8	US-10-750-185-29601	Sequence 29601, A
C 43	21.2	51.7	1015	8	US-10-750-623-29601	Sequence 32429, A
C 44	21.2	51.7	1426	8	US-10-750-185-32429	Sequence 32429, A
C 45	21.2	51.7	1426	8	US-10-750-623-32429	Sequence 32429, A

ALIGNMENTS

RESULT 1
; Sequence 836727, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 836727
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-836727

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Best Local Similarity 76.3%; Pred. No. 10;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4 ACAATGACAAATCAGCTCCCAATACCAAGGCGCTGAC 41
DB 357 AGAAGAGAAACCAAGCTCCCAATATCCAGGCGCTGAC 320

RESULT 2
US-11-136-527-4095
; Sequence 4095, Application US/11136527

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:10:27 ; Search time 2186.62 Seconds
(without alignments)
6758.955 Million cell updates/sec

Title: US-10-500-173-2
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Sequence: 1 gaacaatgacacaatcagc.....gccagagccaccgcgcgcgc 260

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 1176282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_in.*
3: gb_env.*
4: gb_ov.*
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6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vl.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	260	100.0	333	6	BD181249 Cell spec
5	260	100.0	1221	8	D85611 Human smoot
6	260	100.0	142645	8	AC008481 Homo sapi
7	256	98.5	314	8	HS12H4R
8	193.4	74.4	224294	14	AC151861 Colobus g
9	188.2	72.4	178488	14	AC151856 Papio ham
10	184.6	71.0	186803	14	AC151868 Callithri
11	181.4	69.8	181714	14	AC151893 Aotus nan
12	179.8	69.2	250810	14	AC151886 Saimiri b
13	178.2	68.5	163264	14	AC151891 Callicebu
14	168.4	64.8	236017	14	AC150437 Lemur cat
15	164	63.1	1600	8	BC022015 Homo sapi
16	164	63.1	1605	6	CS119457 Sequence
17	150	57.7	1633	8	BC036307 Homo sapi
18	142	54.6	199562	14	AC163457 Bos tauru

C 19	134.2	51.6	207823	14	AC145542
C 20	101	38.8	245942	14	AC132792
C 21	100	38.5	1522	6	E11061
C 22	93.6	36.0	10373	9	MUSH1CA
C 23	93.6	36.0	174533	14	AC073718 Mus muscu
C 24	93.6	36.0	194267	14	AC163623
C 25	93.6	36.0	195294	14	AC051623 Mus muscu
C 26	93.6	36.0	201371	14	AC073786 Mus muscu
C 27	93.6	36.0	236685	14	AC084744 Mus muscu
C 28	92	35.4	1517	6	AX330146 Sequence
C 29	92	35.4	1517	6	AX337316 Sequence
C 30	92	35.4	1517	8	D17408 Homo sapien
C 31	87.4	33.6	485	9	AF123268 Rattus no
C 32	84.2	32.4	3001	9	MMU37071 Mus muscu
C 33	78	30.0	1500	6	CQ724324 Sequence
C 34	78	30.0	1504	6	AX146871 Sequence
C 35	78	30.0	1504	6	AX578072 Sequence
C 36	78	30.0	1504	8	HSU37019 Homo sapien
C 37	77	29.6	1521	8	AK223234 Homo sapi
C 38	76.2	29.3	156	6	CQ503702 Sequence
C 39	76.2	29.3	711	6	CQ482594 Sequence
C 40	74	28.5	1496	8	S80560 basic calpo
C 41	58	22.3	178594	14	AC144892 Didelphis
C 42	56.6	21.8	1216	9	MMCALP01 Mus muscu
C 43	46.2	17.8	165072	4	AC145332 Felis cat
C 44	41.6	16.0	177950	8	AC019103 Homo sapi
C 45	41	15.8	41	6	BD181246 Cell spec

ALIGNMENTS

RESULT 1
BD181247
LOCUS BD181247 260 bp DNA linear PAT 15-MAY-2003
DEFINITION Cell specific express replication vector.
ACCESSION BD181247
VERSION BD181247.1 GI:30792165
KEYWORDS JP 2002335965-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 260)
AUTHORS Takahashi, K., Yamamura, H. and Miyatake, S.
TITLES Cell specific express replication vector
JOURNAL Patent: JP 2002335965-A 2 26-NOV-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002335965-A/2
PD 26-NOV-2002
PF 14-MAY-2001 JP 2001143999
PI KATSUHIITO TAKAHASHI, HISAKO YAMAMURA, SHINICHI MIYATAKE PC
C12N15/09, A61K35/76, A61K48/00, A61P35/00, C12N5/10, C12N15/00, PC
C12N5/00

CC Cell specific express replication vector
FH Key Location/Qualifiers
FT source 1..260
FT /organism='Homo sapiens (human)'.
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source Location/Qualifiers
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/organism='Homo sapiens'
/mol_type='genomic DNA'
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ORIGIN

Query Match 100.0%; Score 260; DB 6; Length 260;
Best Local Similarity 100.0%; Pred. No. 6e-57;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACAATGACACAATCAGCTCCCATACCAAGGCGCTGACATCAAGGGGAGGAG 60
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:04:37 ; Search time 376.877 Seconds
(without alignments)
4597.840 Million cell updates/sec

Title: US-10-500-173-2

Perfect score: 260

Sequence: 1 gaacaatgacacatcagc.....gccagagccaccggccagc 260

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	260	100.0	260	10	ADC21271 Human cel
2	260	100.0	260	10	ADD68310 Human ang
3	260	100.0	260	10	ADD29394 Antiarter
4	260	100.0	260	10	ABZ70045 Oligonuc
5	260	100.0	333	10	ADC21272 Human cel
6	260	100.0	333	10	ADD68311 DNA compr
7	260	100.0	333	10	ADD29395 Human cel
8	260	100.0	333	10	ABZ70046 Human cel
9	213	81.9	1206	13	ACN41242 Human dia
10	213	81.9	1257	13	ACN41241 Human dia
11	213	81.9	1395	13	ACN41239 Human dia
12	213	81.9	1395	13	ACN41240 Human dia
13	164	63.1	1605	12	ADN04009 Antipsori
14	135	51.9	1586	10	ADJ56427 Human cDN
15	100	38.5	1522	2	AAQ86719 Carponin
16	100	38.5	1522	2	AAT18663 Carbonin
17	92	35.4	1517	6	ABL62318 Colon ade
18	92	35.4	1517	6	ABL69488 Prostate
19	92	35.4	1517	6	ABT10830 Human bre

20	78	30.0	1499	12	ADQ83552	Adq83552 Human tum
21	78	30.0	1504	4	AAQ07354	AAQ07354 Human DNA
22	78	30.0	1504	8	ABZ34836	ABZ34836 Coding se
23	78	30.0	1504	10	ADB75245	ADB75245 Prostate
24	78	30.0	1504	13	ADR99030	ADR99030 Calponin
25	76.2	29.3	156	5	ABV35551	ABV35551 Human pro
26	76.2	29.3	711	5	ABV14470	ABV14470 Human pro
27	41	15.8	41	10	ADC21270	ADC21270 Human cel
28	41	15.8	41	10	ADD68309	ADD68309 Human ang
29	41	15.8	41	10	ADD29393	ADD29393 Antiarter
30	41	15.8	41	10	ABZ70044	ABZ70044 Oligonuc
31	40.8	15.7	158001	12	ADL17884	ADL17884 Human pho
32	39.8	15.3	425	9	ACH30634	ACH30634 Human tes
33	39.4	15.2	648	5	ABV05301	ABV05301 Human pro
34	37.6	14.5	142299	10	ADD50651	ADD50651 BAC eseq
35	37.6	14.5	142299	14	ADV77909	ADV77909 Human BAC
36	37.4	14.4	3195	8	ABX75327	ABX75327 Human cDN
37	37.4	14.4	3195	8	ABZ52555	ABZ52555 F2D 8 DNA
38	37.4	14.4	3195	8	ABZ81827	ABZ81827 Receptor
39	37.4	14.4	3195	10	ADB75319	ADB75319 Prostate
40	37.4	14.4	3195	11	ADN39809	ADN39809 Cancer/an
41	37.4	14.4	3195	12	ADO22267	ADO22267 Human F2D
42	37.4	14.4	3195	13	ADR46635	ADR46635 Cancer-as
43	37.4	14.4	3195	14	ADX16340	ADX16340 DNA encod
44	37.4	14.4	3205	12	ADQ24577	ADQ24577 Human sof
45	37.4	14.4	3206	12	ADM86913	ADM86913 Human pro

ALIGNMENTS

RESULT 1

ADC21271
ID ADC21271 standard; DNA; 260 BP.

XX AC ADC21271;

XX DT 18-DEC-2003 (first entry)

XX XX Human cell-specific expression vector-related DNA sequence #2.

DE DE human; cell-specific expression vector; cell-specific replication vector;
KW KW gene therapy; malignant tumour; liver fibrosis; postoperative stenosis;
KW KW organ transplantation; arteriosclerosis; diabetic omentopathy; ds.

XX OS Homo sapiens.

XX PN WO2003057888-A1.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-JP013683.

PR 28-DEC-2001; 2001JP-00402102.

PR 30-AUG-2002; 2002JP-00255395.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Takahashi K, Yamamura H;

XX WPI; 2003-577527/54.

XX Cell-specific expression/replication vector containing transcription
PT initiation regulating domain of human calponin gene, applicable in gene
PT therapy of malignant tumor lung and liver fibrosis or diabetic
PT omentopathy.

PS Claim 3; SEQ ID NO 2; 66pp; Japanese.

XX The invention comprises a cell-specific expression/replication vector
CC which does not act on normal cells. The vector of the invention is useful
CC in gene therapy for the treatment of: malignant tumour, liver fibrosis,
CC postoperative stenosis (e.g. stenosis after organ transplantation),

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:12:09 ; Search time 2672.18 Seconds
(without alignments)
4552.334 Million cell updates/sec

Title: US-10-500-173-2
Perfect score: 260
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	152	58.5	789	3	B1831662	B1831662 603078806
4	112.4	43.2	577	3	B1833410	B1833410 603074509
5	103	39.6	300	1	AU099476	AU099476 AU099476
6	103	39.6	580	3	BP257909	BP257909 BP257909
7	103	39.6	580	3	BP343021	BP343021 BP343021
8	103	39.6	581	3	BP216801	BP216801 BP216801
9	103	39.6	581	3	BP275335	BP275335 BP275335
10	103	39.6	582	3	BP262111	BP262111 BP262111
11	103	39.6	582	3	BP311382	BP311382 BP311382
12	103	39.6	582	3	BP329165	BP329165 BP329165
13	103	39.6	582	3	BP330989	BP330989 BP330989
14	103	39.6	582	3	BP331068	BP331068 BP331068
15	103	39.6	583	3	BP329772	BP329772 BP329772
16	103	39.6	588	3	BP329527	BP329527 BP329527
17	103	39.6	791	1	AU136287	AU136287 AU136287
18	103	39.6	778	1	AU122686	AU122686 AU122686
19	102	39.2	778	8	CX756920	CX756920 AGENCOURT
20	102	39.2	930	5	BUS26756	BUS26756 AGENCOURT
21	101.4	39.0	580	3	BP372922	BP372922 BP372922
22	101.4	39.0	583	3	BP330966	BP330966 BP330966

23	101	38.8	566	3	BP261780	BP261780 BP261780
24	99.8	38.4	582	3	BP206459	BP206459 BP206459
25	97	37.3	581	3	BP328199	BP328199 BP328199
26	94.2	36.2	471	7	CN366947	CN366947 170004241
27	92	35.4	582	3	BP377953	BP377953 BP377953
28	91	35.0	646	7	CN366953	CN366953 170005999
29	91	35.0	1444	4	CR620483	CR620483 full-length
30	90	34.6	742	8	CX752039	CX752039 AGENCOURT
31	88.4	34.0	832	5	BX374338	BX374338 BX374338
32	88.2	33.9	762	8	CX753789	CX753789 AGENCOURT
33	88.2	33.9	1086	3	BM553077	BM553077 AGENCOURT
34	88	33.8	766	1	AL046845	AL046845 DKF2p586B
35	88	33.8	706	1	AL046846	AL046846 DKF2p586B
36	87.4	33.6	714	1	AL046924	AL046924 DKF2p586B
37	87	33.5	996	3	BI771104	BI771104 603059679
38	86.4	33.2	700	1	AL533558	AL533558 AL533558
39	86	33.1	942	5	BUS38479	BUS38479 AGENCOURT
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41	85	32.7	545	6	CD611240	CD611240 56015963H
42	85	32.7	545	6	CD611241	CD611241 56015963J
43	82	31.5	922	8	CV811526	CV811526 AGENCOURT
44	77	29.6	560	3	BP341700	BP341700 BP341700
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ALIGNMENTS

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602696515F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4828610 5',
mRNA sequence.

BG718473
BG718473.1 GI:13997660
EST.

ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 818)
NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10746 row: n column: 03
High quality sequence stop: 798.
Location/Qualifiers
1. 818
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4828610"
/lab_host="DHI08"
/clone_lib="NIH_MGC_97"
/notes="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.2 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein

FEATURES
source

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OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 13:46:44 ; Search time 127.95 Seconds

(without alignments)

3612.096 Million cell updates/sec

Title: US-10-500-173-2

Perfect score: 260

Sequence: 1 gaacaatgacacaatcagc.....gccagagccacggccagc 260

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	78	30.0	1504	3	US-09-949-016-185
5	36.8	14.2	8186	3	US-10-029-517-19
6	36	13.8	120	3	US-09-313-294A-4341
7	34.6	13.3	601	3	US-09-949-016-169734
8	34.6	13.3	3510	3	US-09-265-585C-95
9	34.6	13.3	5962	9	5386025-5
10	34.6	13.3	5975	2	US-08-404-354B-1
11	34.6	13.3	5975	2	US-08-314-083B-1
12	34.6	13.3	5975	2	US-08-435-675B-1
13	34.6	13.3	5975	2	US-08-336-257A-3
14	34.6	13.3	5975	3	US-08-884-599-1
15	34.4	13.2	23187	3	US-09-499-522-1
16	33.4	12.8	601	3	US-09-949-016-169736
17	33.4	12.8	2400	3	US-08-930-001-1
18	33.4	12.8	2400	3	US-09-091-888-1
19	33.4	12.8	18079	3	US-09-949-016-13344
20	33.4	12.8	99748	3	US-09-949-016-11990
21	33.4	12.8	99749	3	US-09-949-016-16518
22	33	12.7	342	3	US-09-893-737-93
23	33	12.7	601	3	US-09-949-016-55187
24	33	12.7	601	3	US-09-949-016-55188

25	33	12.7	601	3	US-09-949-016-169735	Sequence 169735,
26	33	12.7	675	3	US-09-252-991A-5332	Sequence 5532, Ap
27	33	12.7	1485	3	US-09-252-991A-5638	Sequence 5638, Ap
28	33	12.7	3321	3	US-09-252-991A-5668	Sequence 5668, Ap
29	32.6	12.5	690	3	US-09-252-991A-5557	Sequence 5557, Ap
30	32.4	12.5	4403765	3	US-09-103-840A-2	Sequence 2, Appl
31	32.4	12.5	4411529	3	US-09-103-840A-1	Sequence 1, Appl
32	32.2	12.4	7218	2	US-08-232-463-14	Sequence 14, Appl
33	32	12.3	10465	3	US-09-949-016-13136	Sequence 13136, A
34	31.8	12.2	601	3	US-09-949-016-40415	Sequence 40415, A
35	31.8	12.2	601	3	US-09-949-016-91943	Sequence 91943, A
36	31.8	12.2	601	3	US-09-949-016-194884	Sequence 194884,
37	31.8	12.2	601	3	US-09-949-002-3572	Sequence 3572, Ap
38	31.8	12.2	601	3	US-09-949-002-6250	Sequence 6250, Ap
39	31.8	12.2	601	3	US-09-949-002-10314	Sequence 10314, A
40	31.8	12.2	1510	2	US-08-300-903A-12	Sequence 12, Appl
41	31.8	12.2	1510	3	US-08-988-197-12	Sequence 12, Appl
42	31.8	12.2	1510	3	US-10-385-072-12	Sequence 12, Appl
43	31.8	12.2	14395	3	US-09-949-016-12247	Sequence 12247, A
44	31.8	12.2	14395	3	US-09-949-016-16357	Sequence 16357, A
45	31.8	12.2	14688	3	US-09-949-016-12220	Sequence 12220, A

ALIGNMENTS

RESULT 1

US-09-949-016-11927
; Sequence 11927, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11927
; LENGTH: 15585
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(15585)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11927

Query Match	100.0%	Score 260;	DB 3;	Length 15585;
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Matches 260;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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DB	1819	GAACAATGACACATCAGCTCCCAATACCAAGGCGCTGACATCAAGGGGAGGAG 1878		
QY	61	GCAGCTGAGGTGTGGGGGAGGTGCCCCCGCCCTTGCAGCGCCCTACGCAATGGA 120		
DB	1879	GCAGCTGAGGTGTGGGGGAGGTGCCCCCGCCCTTGCAGCGCCCTACGCAATGGA 1938		
QY	121	CGGCGCTGGAAGAGACCCGGGTGCGCTCCGAGCTTCAAAACATGTGAGGAGGAGAG 180		
DB	1939	CGGCGCTGGAAGAGACCCGGGTGCGCTCCGAGCTTCAAAACATGTGAGGAGGAGAG 1998		
QY	181	TGTGAGAGCGGAATTCACGCGCTGCTCTCTTCTACGCTCAGTCCGCCACTCCCCC 240		

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:22:52 ; Search time 610.631 Seconds
(without alignments)
3521.011 Million cell updates/sec

Title: US-10-500-173-2

Perfect score: 260

Sequence: 1 gaacaatgacacatcagc.....gcagagccaccgcccagc 260

Scoring table: IDENTITY_NUC

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	135	51.9	1586	5	US-10-084-817-233
7	92	35.4	1517	3	US-09-969-708-354
8	92	35.4	1517	3	US-09-873-367C-655
9	92	35.4	1517	7	US-10-240-425-1209
10	92	35.4	1517	9	US-10-843-641A-655
11	92	35.4	1517	9	US-10-843-641A-7825
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15	78	30.0	1504	8	US-10-473-974-194
16	78	30.0	1504	10	US-11-051-454-69
17	76.2	29.3	156	8	US-10-357-930-35569
18	76.2	29.3	711	8	US-10-357-930-14461
C 19	42.8	16.5	455	5	US-10-027-632-270660
C 20	42.8	16.5	455	6	US-10-027-632-270660
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C 22	41.6	16.0	455	6	US-10-027-632-270661
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24	41	15.8	41	8	US-10-500-173-1	Sequence 1, Appli
C 25	40.8	15.7	158001	7	US-10-211-179-11	GENERAL INFORMATI
26	39.8	15.3	425	3	US-09-918-995-17846	Sequence 17846, A
27	39.4	15.2	648	8	US-10-357-930-5292	Sequence 5292, Ap
C 28	37.6	14.5	142299	3	US-09-911-077A-14	Sequence 14, Appl
C 29	37.6	14.5	142299	8	US-10-724-806-14	Sequence 14, Appl
C 30	37.4	14.4	3195	5	US-10-205-823-143	Sequence 143, App
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C 32	37.4	14.4	3195	6	US-10-295-027-1127	Sequence 1127, Ap
C 33	37.4	14.4	3195	8	US-10-783-528-48	Sequence 48, Appl
C 34	37.4	14.4	3195	9	US-10-882-586A-8	Sequence 8, Appli
C 35	37.4	14.4	3195	10	US-11-051-454-143	Sequence 143, App
C 36	37.4	14.4	3205	8	US-10-723-860-7397	Sequence 7397, Ap
C 37	37.4	14.4	3206	7	US-10-112-944-6	Sequence 6, Appli
38	37.4	14.4	3740	7	US-10-043-160-4	Sequence 4, Appli
39	37.2	14.3	696	7	US-10-260-238-1452	Sequence 1452, Ap
C 40	36.8	14.2	451	3	US-09-895-828-28	Sequence 28, Appl
C 41	36.8	14.2	451	5	US-10-114-666-28	Sequence 28, Appl
C 42	36.8	14.2	8181	3	US-09-951-938-18	Sequence 18, Appl
C 43	36.8	14.2	8181	7	US-10-447-839A-18	Sequence 18, Appl
C 44	36.8	14.2	8181	8	US-10-778-859-18	Sequence 18, Appl
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ALIGNMENTS

RESULT 1

US-10-477-797-2
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; Publication No. US20040197308A1
; GENERAL INFORMATION:
; APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
; TITLE OF INVENTION: Replication Vector Showing Cell-Specific Expression
; FILE REFERENCE: K01002ECT
; CURRENT APPLICATION NUMBER: US/10/477,797
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: JP P2001-143999
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 260
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-797-2

Query Match		100.0%;	Score 260;	DB 8;	Length 260;
Best Local Similarity		100.0%;	Pred. No. 3.8e-73;		
Matches 260;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GAACAATGACACATCAGCTCCCAATACCAAGGCGCTGACATCACACAGGGGAGGAG 60			
Db	1	GAACAATGACACATCAGCTCCCAATACCAAGGCGCTGACATCACACAGGGGAGGAG 60			
Qy	61	GCAGCTGAGGTTGTGGGGGAGGTGCGCCCGCCCTTGGCAGGCCCTACAGCCAATGGAA 120			
Db	61	GCAGCTGAGGTTGTGGGGGAGGTGCGCCCGCCCTTGGCAGGCCCTACAGCCAATGGAA 120			
Qy	121	CGGCCCTTGGAAAGAGACCCGGGTGCGCTCCGAGCTTCAAAAACATGTGAGGAGGAGAG 180			
Db	121	CGGCCCTTGGAAAGAGACCCGGGTGCGCTCCGAGCTTCAAAAACATGTGAGGAGGAGAG 180			
Qy	181	TGTGACAGCGCACTTACGCGCGCTGCTCTCTCAGCGTCAGTGCAGCCACTGCCCCC 240			
Db	181	TGTGACAGCGCACTTACGCGCGCTGCTCTCTCAGCGTCAGTGCAGCCACTGCCCCC 240			
Qy	241	GCCAGAGCCACCGGCCAGC 260			
Db	241	GCCAGAGCCACCGGCCAGC 260			

RESULT 2

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:36:12 ; Search time 479,811 Seconds

(without alignments)

2167.823 Million cell updates/sec

Title: US-10-500-173-2

Perfect score: 260

Sequence:

1 gaacaatgacacatcagc.....gccagagccaccggccagc 260

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched:

9267905 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SIDS5/ptodata/1/pubpna/US06 NEW PUB.seq.*
- 3: /SIDS5/ptodata/1/pubpna/US07 NEW PUB.seq.*
- 4: /SIDS5/ptodata/1/pubpna/PTC NEW PUB.seq.*
- 5: /SIDS5/ptodata/1/pubpna/US09 NEW PUB.seq.*
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- 13: /SIDS5/ptodata/1/pubpna/US11 NEW PUB.seq.*
- 14: /SIDS5/ptodata/1/pubpna/US11 NEW PUB.seq.*
- 15: /SIDS5/ptodata/1/pubpna/US60 NEW PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	164	63.1	1605	14	US-11-000-688-1504
2	78	30.0	1504	11	US-11-245-147-194
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C 4	36.8	14.2	1582	11	US-11-050-857-464
C 5	36.8	14.2	1582	11	US-11-043-806-59
C 6	34.8	13.4	13299	14	US-11-124-367A-5011
C 7	34.4	13.2	23187	11	US-11-236-198-1
C 8	33.6	12.9	2213	9	US-10-330-773-94
C 9	33.6	12.9	26563	9	US-10-330-773-93
C 10	33.4	12.8	153376	14	US-11-121-086-5
C 11	33.4	12.8	172543	14	US-11-121-086-6
C 12	33.2	12.8	398	11	US-11-116-881A-1686
C 13	33.2	12.8	22855	14	US-11-124-368A-2908
C 14	33	12.7	1521	14	US-11-136-527-1998
C 15	33	12.7	3752	8	US-10-750-185-28772
C 16	33	12.7	3752	8	US-10-750-185-28772
C 17	32.8	12.6	614	6	US-09-925-065A-780929
C 18	32.8	12.6	978	10	US-10-301-480-548844

C 19	32.8	12.6	978	10	US-10-301-480-1162253	Sequence 1162253,
C 20	32.6	12.5	1380	11	US-11-096-568A-21494	Sequence 21494, A
C 21	32.4	12.5	2514	14	US-11-052-554A-543	Sequence 543, App
C 22	32.4	12.5	3071	14	US-11-136-527-2592	Sequence 2592, App
C 23	32.4	12.5	98345	14	US-11-112-908-36	Sequence 36, Appl
C 24	32.2	12.4	670	6	US-09-925-065A-696624	Sequence 696624,
C 25	32.2	12.4	1180	8	US-10-750-185-30591	Sequence 30591, A
C 26	32.2	12.4	1180	8	US-10-750-623-30591	Sequence 30591, A
C 27	32.2	12.4	3939	8	US-10-500-709-1	Sequence 1, Appl
C 28	32	12.3	656	14	US-11-136-527-1651	Sequence 1651, Ap
C 29	32	12.3	656	14	US-11-136-527-5747	Sequence 5747, Ap
C 30	31.6	12.2	598	8	US-10-750-185-4680	Sequence 4680, Ap
C 31	31.6	12.2	598	8	US-10-750-623-4680	Sequence 4680, Ap
C 32	31.6	12.2	126552	14	US-11-121-086-1	Sequence 1, Appl
C 33	31.6	12.2	191684	14	US-11-121-086-2	Sequence 8435, A
C 34	31.4	12.1	2039	9	US-09-925-065A-88435	Sequence 88435, A
C 35	31.4	12.1	2039	9	US-10-301-480-189676	Sequence 189676,
C 36	31.4	12.1	2039	10	US-10-301-480-803085	Sequence 803085,
C 37	31	11.9	591	10	US-10-301-480-532014	Sequence 532014,
C 38	31	11.9	591	10	US-10-301-480-1145423	Sequence 1145423,
C 39	31	11.9	886	8	US-10-750-623-34347	Sequence 34347, A
C 40	31	11.9	886	8	US-10-750-623-34347	Sequence 34347, A
C 41	30.8	11.8	12277	8	US-10-477-507A-3	Sequence 3, Appl
C 42	30.6	11.8	1544	11	US-11-096-568A-24463	Sequence 24463, A
C 43	30.6	11.8	1831	8	US-10-750-185-62445	Sequence 62445, A
C 44	30.6	11.8	1831	8	US-10-750-623-62445	Sequence 62445, A
C 45	30.6	11.8	3090	8	US-10-750-185-44489	Sequence 44489, A

ALIGNMENTS

RESULT 1

US-11-000-688-1504
; Sequence 1504, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNEAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; PRIOR FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1504
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(1605)
; OTHER INFORMATION: calponin 1, basic, smooth muscle(CNN1) gene.
US-11-000-688-1504

Query Match	63.1%	Score	164;	DB	14;	Length	1605;
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Db	6	GCAGGCCCCCTACAGCCCAATGGAACGGCCCTGGAGAGACCCGGTGGCTTCGGAGCTT	65				
QY	157	CAAAAACATGTGAGAGGAGAGAGTGTCGAGACGGAACCTTCAGCGCTCTCTGTCTC	216				
Db	66	CAAAAACATGTGAGAGGAGAGAGTGTCGAGACGGAACCTTCAGCGCTCTCTGTCTC	125				
QY	217	AGCGTCAGTGGCGCCACTGTCCTCCCGCCAGAGCCACCGCCAGC	260				

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:10:27 ; Search time 2800.56 Seconds
(without alignment)
6758.955 Million cell updates/sec

Title: US-10-500-173-3
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Total number of hits satisfying chosen parameters: 11766282

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	323	97.0	1221	8	D85611 Human smoot
5	308	92.5	314	8	HS12H4R
6	261.6	78.6	224294	14	AC151861
7	260	78.1	260	6	BD181247
8	260	78.1	260	6	BD182148
9	259.6	78.0	178488	14	AC151856
10	251.2	75.4	186803	14	AC151868
11	246	74.5	181714	14	AC151893
12	246.4	74.0	163264	14	AC151891
13	246.4	74.0	250810	14	AC151886
14	233.4	70.1	236017	14	AC150437
15	227.8	68.4	1600	8	BC022015
16	227.8	68.4	1605	6	CS119457
17	213.8	64.2	1633	8	BC036307
18	197	59.2	199562	14	AC163457

c 19 195.6 58.7 207823 14 AC145542
20 163.8 49.2 1522 6 E11061
c 21 156.4 47.0 245942 14 AC132792
22 155.8 46.8 1517 6 AX330146
23 155.8 46.8 1517 6 AX337316
24 155.8 46.8 1517 8 D17408
25 145.8 43.8 103733 9 MUSHICA
c 26 145.8 43.8 174533 14 AC073718
27 145.8 43.8 194267 14 AC163623
28 145.8 43.8 195294 14 AC051623
c 29 145.8 43.8 201371 14 AC073786
30 145.8 43.8 236685 14 AC084744
31 141.8 42.6 1500 6 CQ724324
32 141.8 42.6 1504 6 AX146871
33 141.8 42.6 1504 6 AX578072
34 141.8 42.6 1504 8 HSU37019
35 140.8 42.3 1521 8 AK223234
36 136.2 40.9 1496 8 S80560
37 99.4 28.5 1123 4 AF323674
38 89.4 26.8 711 6 CQ482594
39 87.4 26.2 485 9 AF123268
40 86.6 26.0 156 6 CQ503702
41 84.2 25.3 3001 9 MMU37071
42 82.4 24.7 184 9 MMCALP02
43 76.8 23.1 1499 4 AY327118
44 75 22.5 1470 4 SSHICALA
45 72.2 21.7 1524 9 MMHICALA

ALIGNMENTS

RESULT 1
BD181248
LOCUS BD181248 333 bp DNA linear PAT 15-MAY-2003
DEFINITION Cell specific express replication vector.
ACCESSION BD181248
VERSION BD181248.1 GI:30792166
KEYWORDS JP 2002335965-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 333)
AUTHORS Takahashi, K., Yamamura, H. and Miyatake, S.
TITLE Cell specific express replication vector
JOURNAL Patent: JP 2002335965-A 3 26-NOV-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Artificial Sequence
PN JP 2002335965-A/3
PD 26-NOV-2002
PF 14-MAY-2001 JP 2001143999
PI KATSUHIITO TAKAHASHI, HISAKO YAMAMURA, SHINICHI MIYATAKE PC
C12N15/09, A61K35/76, A61K48/00, A61P35/00, C12N5/10, C12N15/00, PC
C12N5/00
CC Description of Artificial Sequence: Region consist of human calponin gene
CC promoter and its structural gene fragment
FH Key Location/Qualifiers
FT source 1. .333
FT Location/Qualifiers
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1. .333
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 76-72; 0; Indels 0; Gaps 0;
Matches 333; Conservative 0; Mismatches 0;
QY 1 GAACAATGCACACATCAGCTCCCATACCAAGGCGCTGACATCACAAGGGGGAAG 60
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GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:04:37 ; Search time 482.692 Seconds
(without alignments)
4597.840 Million cell updates/sec

Title: US-10-500-173-3

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Scoring table: IDENTITY_NUC

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Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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14: Geneseqn2005s.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	333	100.0	333	10	ADD29395	Add29395 Human cal
4	333	100.0	333	10	ABZ70046	Abz70046 Human cal
5	276.8	83.1	1206	13	ACN41242	Acn41242 Human dia
6	276.8	83.1	1257	13	ACN41241	Acn41241 Human dia
7	276.8	83.1	1395	13	ACN41239	Acn41239 Human dia
8	276.8	83.1	1395	13	ACN41240	Acn41240 Human dia
9	260	78.1	260	10	ADC21271	ADC21271 Human cel
10	260	78.1	260	10	ADD68310	Add68310 Human ang
11	260	78.1	260	10	ADD29394	Add29394 Antiarter
12	260	78.1	260	10	ABZ70045	Abz70045 Oligonuci
13	227.8	68.4	1605	12	ADN04009	Adn04009 Antipsoi
14	198.8	59.7	1586	10	ADJ56427	Adj56427 Human cdn
15	163.8	49.2	1522	2	AAQ86719	Aaq86719 Carponin
16	163.8	49.2	1522	2	AAQ86719	Aaq86719 Carponin
17	155.8	46.8	1517	6	ABL62318	AbL62318 Colon ade
18	155.8	46.8	1517	6	ABL69488	AbL69488 Prostate
19	155.8	46.8	1517	6	ABT10830	Abt10830 Human bre

20	141.8	42.6	1499	12	ADQ83552	Adq83552 Human tum
21	141.8	42.6	1504	4	AAO07354	Aao07354 Human DNA
22	141.8	42.6	1504	8	ABZ34836	Abz34836 Coding se
23	141.8	42.6	1504	10	ABW75245	Abw75245 Prostate
24	141.8	42.6	1504	13	ADR99030	Adr99030 Calponin
25	103.6	31.1	425	9	ACH30634	Ach30634 Human tes
26	89.4	26.8	711	5	ABV14470	Abv14470 Human pro
27	86.6	26.0	156	5	ABV35551	Abv35551 Human pro
28	62.4	17.4	538	6	ABN73703	Abn73703 Bovine em
29	57.8	17.4	648	5	ABV05301	Abv05301 Human pro
30	43.6	13.1	120	10	ABX85881	Abx85881 Corn ear-
31	43.4	13.0	1932	6	ABK63774	Abk63774 Rat seque
32	43.4	13.0	1932	10	ADB58375	AdB58375 Toxicity-
33	43.4	13.0	1932	10	ADB52947	AdB52947 Primary r
34	43.4	13.0	1932	13	ADV41198	Adv41198 Rat cardi
35	43.2	13.0	696	12	ADJ40452	Adj40452 Plant cdn
36	41.6	12.5	120	6	ABL71519	AbL71519 Corn tass
37	41.6	12.5	1499	12	ADM86965	Adm86965 Human pro
38	41.2	12.4	283	3	AAC09556	Aac09556 Human sec
39	41.2	12.4	840	14	AEA19761	Aea19761 Novel hum
40	41.2	12.4	1866	12	ADQ64918	Adq64918 Novel hum
41	41.2	12.4	2122	6	ABN95249	Abn95249 Gene #174
42	41.2	12.4	2122	13	ADP54264	Adp54264 Human PRO
43	41.2	12.4	2122	14	ADY14592	Ady14592 DNA encod
44	41.2	12.4	2161	8	ACC46585	Acc46585 Human dit
45	41	12.3	41	10	ADC21270	Adc21270 Human cel

ALIGNMENTS

RESULT 1

ADC21272

ID ADC21272 standard; DNA; 333 BP.

XX AC ADC21272;

XX DT 18-DEC-2003 (first entry)

XX DE Human calponin gene promoter with its structural gene fragment.

XX KW human; cell-specific expression vector; cell-specific replication vector;
 XX KW gene therapy; malignant tumour; liver fibrosis; postoperative stenosis;
 XX KW organ transplantation; arteriosclerosis; diabetic omentopathy; ds;
 XX KW calponin; promoter; structural gene fragment.

XX OS Homo sapiens.

XX FN WO2003057888-A1.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-JP013683.

XX PR 28-DEC-2001; 2001JP-00402102.

XX PR 30-AUG-2002; 2002JP-00255395.

XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX PI Takahashi K, Yamamura H;

XX PI WPI; 2003-577527/54.

XX PT Cell-specific expression/replication vector containing transcription
 XX PT initiation regulating domain of human calponin gene, applicable in gene
 XX PT therapy of malignant tumor lung and liver fibrosis or diabetic
 XX PT omentopathy.

XX PS Claim 4; SEQ ID NO 3; 66pp; Japanese.

XX CC The invention comprises a cell-specific expression/replication vector
 XX CC which does not act on normal cells. The vector of the invention is useful
 XX CC in gene therapy for the treatment of: malignant tumour, liver fibrosis,

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:12:09 ; Search time 3422.44 Seconds
(without alignment)
4552.334 Million cell updates/sec

Title: US-10-500-173-3
Perfect score: 333
Sequence: 1 gaacaatgacacaatcagc.....taagaacaagtaggggtgg 333

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
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2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	273.2	82.0	818	2	BG718473 602696515
2	227.8	68.4	596	2	BG720683 602692572
3	216	64.9	789	3	BI831662 603078806
4	176.2	52.9	577	3	BI831410 603074509
5	166.8	50.1	300	1	AU099476 AU099476
6	166.8	50.1	580	3	BP257909 BP257909
7	166.8	50.1	580	3	BP343021 BP343021
8	166.8	50.1	581	3	BP216801 BP216801
9	166.8	50.1	581	3	BP375335 BP375335
10	166.8	50.1	582	3	BP262111 BP262111
11	166.8	50.1	582	3	BP311382 BP311382
12	166.8	50.1	582	3	BP329165 BP329165
13	166.8	50.1	582	3	BP330989 BP330989
14	166.8	50.1	582	3	BP331068 BP331068
15	166.8	50.1	583	3	BP329772 BP329772
16	166.8	50.1	588	3	BP329527 BP329527
17	166.8	50.1	791	1	AU136287 AU136287
18	166.8	50.1	874	1	AU122686 AU122686
19	165.8	49.8	566	3	BP261780 BP261780
20	165.8	49.8	778	8	CX756920 AGENCOURT
21	165.8	49.8	930	5	BUS26756 AGENCOURT
22	165.2	49.6	580	3	BP372922 BP372922

23	155.2	49.6	583	3	BP330966
24	163.6	49.1	582	3	BP206459
25	160.8	48.3	581	3	BP328199
26	158	47.4	471	7	CN366947
27	155.8	46.8	582	3	BP377953
28	154.8	46.5	646	7	CN366953
29	154.8	46.5	1444	4	CR620483
30	153.8	46.2	742	8	CX752039
31	152	45.6	762	8	CX753789
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33	151.8	45.6	660	1	AL046845
34	151.8	45.6	706	1	AL046846
35	151.2	45.4	714	1	AL046924
36	150.8	45.3	996	3	BI771104
37	149.8	45.0	700	1	AL533558
38	149.8	45.0	942	5	BU838479
39	148.8	44.7	545	6	CD611240
40	148.8	44.7	545	6	CD611241
41	143.6	43.1	922	8	CV811526
42	141.2	42.4	832	5	BX374338
43	140.8	42.3	560	3	BP341700
44	140.8	42.3	566	3	BP377279
45	140.8	42.3	580	3	BP372484

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
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mRNA sequence.
ACCESSION
BG718473
VERSION
BG718473.1 GI:13997660
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 818)
NIH-MGC <http://mgc.ncl.nih.gov/>.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10746 row: n column: 03
High quality sequence stop: 798.

FEATURES
source

1..818
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4828610"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescript (modified
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(gtcgag); Oligo-dT primed using primer
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insert size 2.2 Kb and normalized to 10^5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein

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OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 13:46:44 ; Search time 163.874 Seconds
(without alignments)
3612.096 Million cell updates/sec

Title: US-10-500-173-3
Perfect score: 333
Sequence: 1 gaacaatgacacacagc.....taagaacaagggtgggtgg 333

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	44.4	13.3	15273	3	US-09-949-016-12006
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9	43.6	13.1	120	3	US-09-949-016-13341
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12	41.2	12.4	2122	3	US-09-949-016-1599
13	40.6	12.2	1589	3	US-09-949-016-1599
14	40.6	12.2	1607	3	US-09-949-016-1599
15	36.8	11.1	8186	3	US-09-949-016-1264
16	36.2	10.9	23187	3	US-09-949-016-1264
17	34.6	10.4	601	3	US-09-949-016-169734
18	34.6	10.4	3510	3	US-09-949-016-169734
19	34.6	10.4	5962	9	US-09-949-016-169734
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21	34.6	10.4	5975	2	US-08-314-083B-1
22	34.6	10.4	5975	2	US-08-435-675B-1
23	34.6	10.4	5975	2	US-08-336-257A-3
24	34.6	10.4	5975	3	US-08-884-599-1

Sequence 32, Appl
Sequence 7188, Ap
Sequence 667, App
Sequence 15078, A
Sequence 13607, A
Sequence 12340, A
Sequence 12220, A
Sequence 13719, A
Sequence 13538, A
Sequence 19, Appl
Sequence 169736
Sequence 1, Appl
Sequence 17005, A
Sequence 13344, A
Sequence 13217, A
Sequence 11990, A
Sequence 16516, A
Sequence 118, Appl
Sequence 93, Appl
Sequence 55187, A

ALIGNMENTS

RESULT 1
US-09-949-016-11927
; Sequence 11927, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11927
; LENGTH: 15585
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(15585)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11927

Query Match 99.5%; Score 331.4; DB 3; Length 15585;
Best Local Similarity 99.7%; Pred. No. 5.6e-83;
Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1819 GAAACAATGACACATCAGCTCCCAATCAAGGGCCTGCATCAACAGGGGAGGGAAG 1878
QY 61 GCAGCTGAGGTGTGGGGGAGGTCCCGCCCTTGGCAGGCCCTCAGCCCAATGGAA 120
DB 1879 GCAGCTGAGGTGTGGGGGAGGTCCCGCCCTTGGCAGGCCCTCAGCCCAATGGAA 1938
QY 121 CGGCCCTTGAAGAGACCCGGGTCCGCTCCGAGCTTCAAAAACATGTGAGGAGGGAAG 180
DB 1939 CGGCCCTTGAAGAGACCCGGGTCCGCTCCGAGCTTCAAAAACATGTGAGGAGGGAAG 1998
QY 181 TGTGAGAGCGGAACCTTACAGCGCTCCTCTGTGTCTCAGCGTCACTGCCCTTGCCTCC 240

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:22:52 ; Search time 782.077 Seconds
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3521.011 Million cell updates/sec

Title: US-10-500-173-3
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	333	100.0	333	8	US-10-500-173-3
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4	260	78.1	260	8	US-10-500-173-2
5	206.8	62.1	1580	6	US-10-062-674-1778
6	198.8	59.7	1586	5	US-10-084-817-233
7	155.8	46.8	1517	3	US-09-969-708-354
8	155.8	46.8	1517	3	US-09-873-367C-655
9	155.8	46.8	1517	7	US-10-240-425-1209
10	155.8	46.8	1517	9	US-10-843-641A-655
11	155.8	46.8	1517	9	US-10-843-641A-7825
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16	141.8	42.6	1504	10	US-11-051-454-69
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24	43.2	13.0	696	7	US-10-260-238-1452	Sequence 1452, Ap
c 25	42.8	12.9	455	5	US-10-027-632-270660	Sequence 270660, Ap
c 26	42.8	12.9	455	6	US-10-027-632-270660	Sequence 270660, Ap
c 27	41.6	12.5	120	3	US-09-294-093B-893	Sequence 893, App
c 28	41.6	12.5	455	5	US-10-027-632-270661	Sequence 270661, Ap
c 29	41.6	12.5	455	6	US-10-027-632-270661	Sequence 270661, Ap
30	41.6	12.5	1499	7	US-10-112-944-58	Sequence 58, Appl
31	41.2	12.4	2122	3	US-09-880-107-1747	Sequence 1747, Ap
32	41	12.3	41	8	US-10-477-797-1	Sequence 1, Appl1
33	41	12.3	41	8	US-10-500-173-1	Sequence 1, Appl1
34	41	12.3	127	3	US-09-294-093B-5323	Sequence 5323, Ap
c 35	40.8	12.3	158001	7	US-10-211-173-11	GENERAL INFORMATION
c 36	40.8	12.2	419	3	US-09-960-352-12371	Sequence 12371, A
c 37	40.6	12.2	648	3	US-09-969-034-2416	Sequence 2416, Ap
c 38	40.6	12.2	1607	3	US-09-795-651-94	Sequence 94, Appl
c 39	40.6	12.2	1607	6	US-10-133-937-43	Sequence 43, Appl
c 40	40.6	12.2	1607	6	US-10-172-118-679	Sequence 679, Appl
c 41	40.6	12.2	1607	6	US-10-159-563-43	Sequence 43, Appl
c 42	40.6	12.2	1607	7	US-10-342-887-679	Sequence 679, Appl
c 43	40.6	12.2	1607	9	US-10-756-149-40	Sequence 40, Appl
c 44	37.6	11.3	142299	3	US-09-911-077A-14	Sequence 14, Appl
c 45	37.6	11.3	142299	8	US-10-724-806-14	Sequence 14, Appl

ALIGNMENTS

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; Sequence 3, Application US/10477797
; Publication NO. US20040197308A1
; GENERAL INFORMATION:
; APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
; TITLE OF INVENTION: Replication Vector Showing Cell-Specific Expression
; FILE REFERENCE: K01002PCT
; CURRENT APPLICATION NUMBER: US/10/477,797
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: JP P2001-143999
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Region consist
; OTHER INFORMATION: of human calpain gene promoter and its structural
; OTHER INFORMATION: gene fragment
US-10-477-797-3

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				Indels	0;
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Qy	121	CGGCCCTTGGAGAGACCCGGGTGCGCTCCGAGCTTCAAAACATGTGAGGAGGAGAG	180		
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 02:36:12 ; Search time 614.527 Seconds
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2167.823 Million cell updates/sec

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3: /SID55/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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SUMMARIES

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4	44.6	13.4	2271	14	US-11-136-527-2536
5	44.4	13.3	168516	14	US-11-121-086-3
6	40.6	12.2	736	8	US-10-750-185-61962
7	40.6	12.2	736	8	US-10-750-623-61962
8	40.6	12.2	1607	14	US-11-000-688-1008
9	40.2	12.1	1400	14	US-11-136-527-7127
10	36.8	11.1	1084	9	US-10-517-696-82
11	36.8	11.1	1582	11	US-11-050-857-464
12	36.8	11.1	1582	11	US-11-043-806-59
13	36.2	10.9	23187	11	US-11-236-138-1
14	35.8	10.8	627	10	US-10-301-480-239363
15	35.8	10.8	627	10	US-10-301-480-852772
16	35.8	10.8	635	6	US-09-925-065A-144853
17	35.8	10.8	780	10	US-10-301-480-542693
18	35.8	10.8	780	10	US-10-301-480-1156102

C	19	34.8	10.5	13299	14	US-11-124-367A-5011	Sequence 5011, Ap
	20	33.6	10.1	2213	9	US-10-330-773-94	Sequence 94, Appl
	21	33.6	10.1	22855	14	US-11-124-368A-2908	Sequence 2908, Ap
	22	33.6	10.1	26563	9	US-10-330-773-93	Sequence 93, Appl
C	23	33.6	10.1	168516	14	US-11-121-086-3	Sequence 3, Appl
C	24	33.4	10.0	153376	14	US-11-121-086-5	Sequence 5, Appl
C	25	33.4	10.0	172543	14	US-11-121-086-6	Sequence 6, Appl
	26	33.2	10.0	398	11	US-11-116-881A-1686	Sequence 1686, Ap
C	27	33	9.9	1521	14	US-11-136-527-1398	Sequence 1998, Ap
	28	33	9.9	3752	8	US-10-750-185-28772	Sequence 28772, A
	29	33	9.9	3752	8	US-10-750-623-28772	Sequence 28772, A
C	30	32.8	9.8	614	6	US-09-925-065A-780929	Sequence 780929, A
	31	32.8	9.8	656	14	US-11-136-527-1651	Sequence 1651, Ap
C	32	32.8	9.8	656	14	US-11-136-527-747	Sequence 5747, Ap
C	33	32.8	9.8	978	10	US-10-301-480-548844	Sequence 548844, A
C	34	32.8	9.8	978	10	US-10-301-480-1162253	Sequence 1162253, A
C	35	32.6	9.8	1380	11	US-11-096-568A-21494	Sequence 21494, A
	36	32.4	9.7	554	6	US-09-925-065A-527354	Sequence 527354, A
C	37	32.4	9.7	2514	14	US-11-052-554A-543	Sequence 543, App
	38	32.4	9.7	3071	14	US-11-136-527-2592	Sequence 2592, App
	39	32.4	9.7	98345	14	US-11-112-908-36	Sequence 36, Appl
	40	32.2	9.7	670	6	US-09-925-065A-696624	Sequence 696624, A
C	41	32.2	9.7	1180	8	US-10-750-185-30591	Sequence 30591, A
C	42	32.2	9.7	1180	8	US-10-750-623-30591	Sequence 30591, A
C	43	32.2	9.7	3939	8	US-10-500-709-1	Sequence 1, Appl
	44	31.8	9.5	583	6	US-09-925-065A-502074	Sequence 502074, A
	45	31.8	9.5	1924	7	US-10-782-413-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-11-000-688-1504
; Sequence 1504, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1433-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; PRIOR FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1504
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; NAME/KEY: misc feature
; LOCATION: (1)..(1605)
; OTHER INFORMATION: calponin 1, basic, smooth muscle (CNN1) gene.
US-11-000-688-1504

QY	97	GGCAGGCCCTACAGCCCAATGGAACGGCCCTGGGAAGACACCGGGTGCCTCCGAGCTT	156
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QY	157	CAAAAACATGTGAGGAGGAAGAGTGTGCACACCGAACTTCAGCGCTGCTCTCTTC	216
DB	66	CAAAAACATGTGAGGAGGAAGAGTGTGCACACCGAACTTCAGCGCTGCTCTCTTC	125
QY	217	AGCGTCAGTGGCGCCCACTGCGCCCGCCAGAGACCCACCGGCGAGCATGTCTCTGCTCACT	276